10038.177

Freeform Search

Database: US Pre-Grant Publication Full-Text Database; US Patents Full-Text Database; US OCR Full-Text Database; EPO Abstracts Database; JPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: l2 and reverse transcri$5

Display: 10 **Documents in Display Format:** - **Starting with Number** 1

Generate: ○ Hit List ◉ Hit Count ○ Side by Side ○ Image

Search Clear Interrupt

Search History

DATE: Thursday, April 08, 2004 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L4	l2 and reverse transcri$5	1	L4
L3	L2 and reverse trancri$5	0	L3
L2	L1 and (length or base pair or nucleotide$1)	3	L2
L1	single strand$2 near5 binding protein$1 near5 cDNA	3	L1

END OF SEARCH HISTORY

Freeform Search

10038,177

Database: US Pre-Grant Publication Full-Text Database; US Patents Full-Text Database; US OCR Full-Text Database; EPO Abstracts Database; JPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: 14 and single strand binding protein

Display: 10 **Documents in Display Format:** - **Starting with Number** 1

Generate: ○ **Hit List** ◉ **Hit Count** ○ **Side by Side** ○ **Image**

Search | Clear | Interrupt

Search History

DATE: Thursday, April 08, 2004 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L6	l4 and single strand binding protein	1	L6
L5	L4 and (cDNA near5 length)	0	L5
L4	baugh.in.	753	L4
L3	L2 and cDNA	10	L3
L2	L1 and binding protein$1	16	L2
L1	hunter.in.	7017	L1

END OF SEARCH HISTORY

10/038,177

Freeform Search

Database: US Pre-Grant Publication Full-Text Database; US Patents Full-Text Database; US OCR Full-Text Database; EPO Abstracts Database; JPO Abstracts Database; Derwent World Patents Index; IBM Technical Disclosure Bulletins

Term: l4 and cDNA

Display: 10 **Documents in Display Format:** - **Starting with Number** 1

Generate: ○ **Hit List** ◉ **Hit Count** ○ **Side by Side** ○ **Image**

Search | Clear | Interrupt

Search History

DATE: Thursday, April 08, 2004 Printable Copy Create Case

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ			
L5	l4 and cDNA	8	L5
L4	L3 and bacteriophage$1	8	L4
L3	L2 and reverse transcrib$3	14	L3
L2	L1 and (cDNA near5 length)	117	L2
L1	single strand$2 near5 binding protein$1	553	L1

END OF SEARCH HISTORY

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FILE 'CAPLUS' ENTERED AT 12:06:38 ON 08 APR 2004
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FILE 'EMBASE' ENTERED AT 12:06:38 ON 08 APR 2004
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=> s hunter.in.
L1       12879 HUNTER.IN.

=> s l1 and single-strand##
L2          84 L1 AND SINGLE-STRAND##

=> s l2 and ((mak### or synthsiz###) (10a) cDNA)
L3           0 L2 AND ((MAK### OR SYNTHSIZ###) (10A) CDNA)

=> s l2 and binding protein#
L4           0 L2 AND BINDING PROTEIN#

=>

=> s l1 and binding protein#
L5         161 L1 AND BINDING PROTEIN#

=> s l5 and single-strand##
L6           0 L5 AND SINGLE-STRAND##

=> s l1 and single strand## binding protein#
L7           0 L1 AND SINGLE STRAND## BINDING PROTEIN#

=> s baugh.in.
L8          44 BAUGH.IN.

=> s l8 and reverse transcrib###
L9           1 L8 AND REVERSE TRANSCRIB###

=> d l9  bib ab kwic

L9   ANSWER 1 OF 1  BIOSIS  COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN   2002:198844  BIOSIS
DN   PREV200200198844
TI   A global survey of transcriptional targets of the AML-associated homeobox
     protein, HOXA9, using cDNA microarray analysis.
AU   Dorsam, Sheri [Reprint author]; Haqq, Christopher; Bernstein, Hillary;
     Largman, Corey [Reprint author]; Lawrence, H. Jeffrey [Reprint author]
CS   Dept. of Medicine, Veterans Affairs Medical Center, San Francisco, CA, USA
SO   Blood, (November 16, 2001) Vol. 98, No. 11 Part 1, pp. 285a. print.
     Meeting Info.: 43rd Annual Meeting of the American Society of Hematology,
     Part 1. Orlando, Florida, USA. December 07-11, 2001. American Society of
     Hematology.
     CODEN: BLOOAW. ISSN: 0006-4971.
DT   Conference; (Meeting)
     Conference; Abstract; (Meeting Abstract)
     Conference; (Meeting Poster)
LA   English
ED   Entered STN: 20 Mar 2002
     Last Updated on STN: 20 Mar 2002
AB   HOX homeodomain proteins are master regulators of embryonic development,
```

and they play important roles in normal and leukemic hematopoiesis. Mice with a targeted disruption of the HOXA9 gene have a variety of myeloid and lymphoid defects. Conversely, enforced over-expression of HOXA9 in mouse marrow cells leads to the development of acute myelogenous leukemia (AML), and the HOXA9 gene is activated in most cases of human AML. Although HOXA9 encodes a DNA-binding protein, a paucity of information exists concerning its direct downstream target genes, and whether or not it is a transcriptional activator or repressor. In order to identify genes which are directly regulated by HOXA9 in blood cells, HOXA9 was transiently over-expressed in three human leukemic cell lines, U937 (myelomonocytic), K562 (erythroid-megakaryocytic), and Jurkat (T lymphocytic). Cells were transfected with vectors expressing either HOXA9 and GFP or GFP alone. GFP-expressing cells were sorted by FACS 24 hours after transfection, and RNA and protein were isolated. High levels of HOXA9 mRNA and protein expression were confirmed by quantitative real time RT-PCR and Western blot analyses. mRNA from HOXA9-expressing and control, transfected cells was **reverse transcribed** and amplified following a protocol described by **Baugh** et. al. This procedure includes synthesizing double-stranded cDNA and T7 RNA Polymerase driven in vitro transcription steps. Amplified RNA was labeled with Cy3 (control) and Cy5 (+HOXA9) fluorescent dyes. The labeled samples were combined and hybridized to high density large-scale cDNA microarrays containing 41,000 human clones from Research Genetics (Huntsville, AL). To determine if this amplification method faithfully reflects mRNA levels present in unamplified total RNA, control experiments were performed to compare Cy5/Cy3 ratios in unamplified sample hybridizations with ratios in amplified sample hybridizations. Gene expression changes between the two RNA sample types correlated well, with a coefficient of 0.75. Hybridization-to-hybridization variability was also analyzed and the correlation coefficient was 0.85 between replicate hybridizations of amplified or unamplified samples. In HOXA9 experiments, preliminary analysis of six hybridizations consisting of two replicates from each cell line, and scoring gene targets that were at least 2.5 fold up- or down-regulated, revealed that HOXA9 appears to modulate the expression of many genes. Putative HOXA9 targets include oncogenic transcription factors (Fos/Jun family members), oncogenic signaling molecules, metabolic enzymes (aldehyde dehydrogenases and carboxypeptidases), cell surface molecules (CD36), RNA binding proteins and processing enzymes, and proteins involved in ubiquitination and proteolysis, such as von Hippel-Lindau tumor suppressor protein and several proteasome 26S subunits. Interestingly, some genes showed contrasting expression patterns in different cell lines, e.g. down-regulation in U937 and K562 cells, but up-regulation in Jurkat cells, suggesting that the transcriptional effects of HOXA9 depend on cellular context. These data indicate that HOXA9 positively and negatively regulates the expression of a variety of genes, some in a cell-specific manner and others more universally. A comprehensive analysis of the transcriptome of the HOXA9 gene in hematopoietic cells will be presented.

AB. . . expression were confirmed by quantitative real time RT-PCR and Western blot analyses. mRNA from HOXA9-expressing and control, transfected cells was **reverse transcribed** and amplified following a protocol described by **Baugh** et. al. This procedure includes synthesizing double-stranded cDNA and T7 RNA Polymerase driven in vitro transcription steps. Amplified RNA was. . .

```
=> s single strand##(10a)binding protein#(10a)cDNA
L10         55 SINGLE STRAND##(10A) BINDING PROTEIN#(10A) CDNA

=> s l10 and reverse transcri########
L11          5 L10 AND REVERSE TRANSCRI########

=> s l11 and (length or base pair###)
L12          0 L11 AND (LENGTH OR BASE PAIR###)
```

=> dup rem l11
PROCESSING COMPLETED FOR L11
L13 2 DUP REM L11 (3 DUPLICATES REMOVED)

=> d l13 1-2 bib ab kwic

L13 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1
AN 2003:904030 CAPLUS
DN 140:55256
TI Enhancement of DNA, **cDNA** synthesis and fidelity at high temperatures by a dimeric **single-stranded** DNA-**binding protein**
AU Perales, Celia; Cava, Felipe; Meijer, Wilfried J. J.; Berenguer, Jose
CS Centro de Biologia Molecular Severo Ochoa, Consejo Superior de Investigaciones Cientificas-Universidad Autonoma de Madrid, Campus de Cantoblanco, Madrid, 28049, Spain
SO Nucleic Acids Research (2003), 31(22), 6473-6480
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB Bacterial single-stranded DNA-binding proteins (SSBs) are required for DNA replication and repair. We have over-expressed and purified the native form and two His-tagged fusions of the SSB from Thermus thermophilus (TthSSB). The three proteins were found as dimers in solution They bound in vitro to single-stranded DNA specifically over a temperature range of 4-80°, and the wild-type protein could withstand incubation at 94° for 2 min. Addition of TthSSB to PCR halved the elongation time required for the DNA polymerases of T.thermophilus (Tth) and Pyrococcus furiosus (Pfu) to synthesize DNA fragments in PCRs. The presence of TthSSB increased the fidelity of the proof-reading-free DNA polymerase of T.thermophilus. TthSSB was also able to bind single-stranded RNA, allowing a dramatic enhancement of the **reverse transcription** activity of its cognate Tth DNA polymerase during cDNA synthesis.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT
TI Enhancement of DNA, **cDNA** synthesis and fidelity at high temperatures by a dimeric **single-stranded** DNA-**binding protein**
AB Bacterial single-stranded DNA-binding proteins (SSBs) are required for DNA replication and repair. We have over-expressed and purified the native form and two His-tagged fusions of the SSB from Thermus thermophilus (TthSSB). The three proteins were found as dimers in solution They bound in vitro to single-stranded DNA specifically over a temperature range of 4-80°, and the wild-type protein could withstand incubation at 94° for 2 min. Addition of TthSSB to PCR halved the elongation time required for the DNA polymerases of T.thermophilus (Tth) and Pyrococcus furiosus (Pfu) to synthesize DNA fragments in PCRs. The presence of TthSSB increased the fidelity of the proof-reading-free DNA polymerase of T.thermophilus. TthSSB was also able to bind single-stranded RNA, allowing a dramatic enhancement of the **reverse transcription** activity of its cognate Tth DNA polymerase during cDNA synthesis.
ST single stranded DNA binding protein polymerase **reverse transcription**; gene sequence Thermus single stranded DNA binding protein SSB
IT Molecular association
(DNA-SSB; dimeric single-stranded DNA-binding protein from Thermus thermophilus binds to single-stranded RNA and single-stranded DNA and promotes transcription and **reverse transcription** activity of DNA polymerase)
IT Thermus thermophilus

(SSB gene sequence; dimeric single-stranded DNA-binding protein from Thermus thermophilus binds to single-stranded RNA and single-stranded DNA and promotes transcription and **reverse transcription** activity of DNA polymerase)

IT DNA repair
Reverse transcription
(dimeric single-stranded DNA-binding protein from Thermus thermophilus binds to single-stranded RNA and single-stranded DNA and promotes transcription and **reverse transcription** activity of DNA polymerase)

IT RNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(dimeric single-stranded DNA-binding protein from Thermus thermophilus binds to single-stranded RNA and single-stranded DNA and promotes transcription and **reverse transcription** activity of DNA polymerase)

IT DNA sequences
(of Thermus thermophilus ssb gene; dimeric single-stranded DNA-binding protein from Thermus thermophilus binds to single-stranded RNA and single-stranded DNA and promotes transcription and **reverse transcription** activity of DNA polymerase)

IT Protein sequences
(of Thermus thermophilus ssb; dimeric single-stranded DNA-binding protein from Thermus thermophilus binds to single-stranded RNA and single-stranded DNA and promotes transcription and **reverse transcription** activity of DNA polymerase)

IT DNA formation
(replication; dimeric single-stranded DNA-binding protein from Thermus thermophilus binds to single-stranded RNA and single-stranded DNA and promotes transcription and **reverse transcription** activity of DNA polymerase)

IT Proteins
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(single-stranded DNA-binding, gene ssb; dimeric single-stranded DNA-binding protein from Thermus thermophilus binds to single-stranded RNA and single-stranded DNA and promotes transcription and **reverse transcription** activity of DNA polymerase)

IT DNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(single-stranded; dimeric single-stranded DNA-binding protein from Thermus thermophilus binds to single-stranded RNA and single-stranded DNA and promotes transcription and **reverse transcription** activity of DNA polymerase)

IT Gene, microbial
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(ssb, sequence; dimeric single-stranded DNA-binding protein from Thermus thermophilus binds to single-stranded RNA and single-stranded DNA and promotes transcription and **reverse transcription** activity of DNA polymerase)

IT 606683-70-9
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; dimeric single-stranded DNA-binding protein from Thermus thermophilus binds to single-stranded RNA and single-stranded DNA and promotes transcription and **reverse transcription** activity of DNA polymerase)

IT 9012-90-2, DNA polymerase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(dimeric single-stranded DNA-binding protein from Thermus thermophilus binds to single-stranded RNA and single-stranded DNA and promotes transcription and **reverse transcription** activity of DNA polymerase)

IT 606683-69-6, GenBank AJ564626
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; dimeric single-stranded DNA-binding protein from Thermus thermophilus binds to single-stranded RNA and single-stranded DNA and promotes transcription and **reverse transcription** activity of DNA polymerase)

L13 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:616261 CAPLUS
DN 137:151099
TI Method and test kits for quantitative mRNA amplification by in vitro transcription
IN Hunter, Craig P.; Baugh, Larry Ryan
PA USA
SO U.S. Pat. Appl. Publ., 17 pp.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002110827	A1	20020815	US 2001-38177	20011221
US 2001-268102P	P	20010212		

AB The present invention relates to methods for copying and amplifying complex populations of mRNA mols. Specifically, the invention relates to methods for copying and amplifying complex populations of mRNA mols. that maximize the retention of representative information in populations of copied mRNA mols. Effective transcript profiling in animal systems requires isolation of homogeneous tissue or cells followed by faithful mRNA amplification. Linear amplification based on cDNA synthesis and in vitro transcription is reported to maintain representation of mRNA levels, however, quant. data demonstrating this as well as a description of inherent limitations is lacking. Published protocols produce a template-independent product in addition to amplifying real target mRNA thus reducing the specific activity of the final product. A modified amplification protocol that minimizes the generation of template-independent product and can therefore generate the desired microgram quantities of message-derived material from 100 ng of total RNA are described. Application of a second, nested round of cDNA synthesis and in vitro transcription reduces the required starting material to 2 ng of total RNA. Quant. anal. of these products on Caenorhabditis elegans Affymetrix GeneChips shows that this amplification does not reduce overall sensitivity and has only minor effects on fidelity.

IT PCR (polymerase chain reaction)
(RT-PCR (**reverse transcription**-PCR); method and test kits for quant. mRNA amplification by in vitro transcription)

IT Coliphage T4
(gp32 **single-stranded** DNA **binding protein** for **cDNA** synthesis; method and test kits for quant. mRNA amplification by in vitro transcription)

IT 9068-38-6, **Reverse transcriptase**
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(for cDNA synthesis; method and test kits for quant. mRNA amplification by in vitro transcription)

=>